SEQUENCE LISTING

<110> WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
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Watts, Jennifer L.

<120> DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF POLYUNSATURATED FATTY ACIDS

<130> 4630-58963

<140> US 09/857,583
<141> 2001-06-05

<150> US 60/111,301
<151> 1998-12-07

<150> PCT/US99/28655
<151> 1999-12-06

<160> 13

<170> PatentIn version 3.2

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<212> DNA
<213> Caenorhabditis elegans

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ctgagatcac atccaggtgg tagtgcaatt actacctata aaaatatgga tgccactacc 180

gtattccaca cattccatac tggttctaaa gaagcgtatc aatggctgac agaattgaaa 240

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caataccaca catattatct tccatcagct attctaatgg gagttgcgtg gcaacaattg 540

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Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
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His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
50 55 60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
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Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu

100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
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Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
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Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
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Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
325 330 335

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Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
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Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
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Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
385                 390                 395                 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
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Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
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gctcaagcgc atgcccaaaa tcaatcccag ttctgagttg ccaccccagg ctgcagtgaa    240

tgaagctcaa gaggatttcc ggaagctccg agaagagttg atcgcaactg gcatgtttga    300

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ctatcaacag atgggctggc tttctcatga catttgccac caccagactt tcaagaaccg    480

gaactggaac aacctcgtgg gactggtatt tggcaatggt ctgcaaggtt tttccgtgac    540

atggtggaag gacagacaca atgcacatca ttcggcaacc aatgttcaag ggcacgaccc    600

tgatattgac aacctccccc tcttagcctg gtctgaggat gacgtcacac gggcgtcacc    660
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ccaggtggaa cagctgtgcc agaagcacaa cctgccgtat cggaacccgc tgccccatga 1200

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Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
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Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
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Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
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His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
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Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
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Trp Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
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Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
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Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
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Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
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Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
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Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
            260                 265                 270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
        275                 280                 285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
    290                 295                 300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
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Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
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Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
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Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
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His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
370 375 380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
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X = any amino acid

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X = any amino acid

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Gln Xaa Xaa His His

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